Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID:1)



1 GATCACAGTC TITTGTATTIT TCTACTICG CCTTTAGCTG TCCCTTTGG TCTCGAAGTG

61 AAGAAAGCTC TTTTGCTAGC CTGGTTCGCT CTTCCGTTTC ACATCGGCCA ATTTTAGCTT 121 TCTCAATGCT TTTCTGTAGG CTTGCATGCT TTTGACTTCC CTCAGACAAC TGAGATTCCA

181 GAACCTCCAA CTTATGTTTC CTTGCATGAA GAGCTTTACT TGGAAAAGCC CAATAATAAT

241 TAGAAGTTCC GATC

Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO:2) and amino acid sequence (SEQ ID. NO:3) of 121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

1	cc	aaa	atc	aaa	cgc	gtc	egg	gcc	tgt	ece	gcc	cct	ctc	ccca	aag	ege	ggg	ccc	ggc	cagc
1								М	s	K	K	K	G	L	S	Α	E	E	K	R
61	gg	aag	ccc	ctg	cgc	ccg	ege	CAT	GTC/	AAA	GAA	AAA	AGG	ACTO	GAG.	rgc	4GA	AGA.	AAA	GAGA
14	Т	R	М	М	E	I	F	S	E	T	K	D	٧	F	Q	L	K	D	L	E
121	AC'	rcg	CAT	GAT	GGA	AATA	TT	rtc'	rga/	AAC?	AAA	AGA'	TGT	ATT	rca/	ATT	AAA	\GA(CTT	GGAG
34	K	I	Α	P	K	E	K	G	1	Т	А	М	s	V	K	E	v	L	Q	s
181	AA	GAT'	rgc'	TCC	CAA	AGA(SAA	AGG	CAT	rac'	rgc'	rat	GTC	AGT/	\AA	\GA	AGT	CT	rca.	AAGC
54	L	٧	D	D	G	М	v	D	С	E	R	Ι	G	Т	s	N	Y	Y	W	A
241	TT	AGT'	rga'	TGA	TGG'	rato	GT'	rga(CTG:	rgac	SAG	GAT	CGG	AAC:	rrc:	raa'	rta:	rta'	ГТG	GGCT
74	F	P	s	K	Α	L	Н	Α	R	K	Н	K	L	E	V	L	E	s	Q	L
301	TT'	rcc.	AAG'	TAA.	AGC'	rct:	rca:	rgc	AAG	SAAA	ACA'	raa	STT	GGA	GGT'	гсто	GGA/	ATC:	rca(GTTG
94	s	E	G	s	Q	K	Н	А	s	L	Q	K	S	I	E	K	А	K	I	G
361	TC	rga	GGG	AAG	TCA	AAA	GCA'	rgc	AAG	CCTA	ACA	GAA	AAG	CAT	rgad	SAA	AGC'	(AA	\AT	rggc
114	R	С	Ε	T	E	Ε.	R	т	R	L	А	K	E	L	s	s	L	R	D	Q
421	CG	ATG'	rga.	AAC	GGA	AGA	GCG2	AAC	CAGO	GCT?	AGC	AAA	AGA	GCT:	rrc:	TC	ACT:	CG	\GA(CCAA
134	R	E	Q	\mathbf{L}	K	A	E	V	E	K	γ.	K	D	С	D	P	Q	v	v	E
481	AG	GGA.	ACA	GCT.	AAA	GGC/	\GA/	AGTA	AGA/	\AAA	ATA	CAA	AGA(CTGT	rga:	CCC	GCA <i>I</i>	AGT'	rgte	GGAA
154	Ε	1	R	Q	A	N	K	v	Α	K	E	A	Α	N	R	W	Т	D	N	I
541	GA	AAT	ACG(CCA	AGC	\AA'	(AA)	AGT	AGC	CAA	\GAJ	AGC'	rgci	raac	CAG	ATG	GAC'	'GA'	гаас	CATA
174	F	A	I	K	s	W	Α	K	R	K	F	G	F	E	E	N	K	1	D	R
601	TT	CGC	AAT	AAA.	ATC:	rtgo	GCC	CAA	AAG!	AAA	ATT:	rgg	STTI	rga,	AGA/	AA!	raa <i>i</i>	AT'	rga:	ГАGA
194	Т	F	G	I	P	E	D	F	D	Y	Ι	D	*							
661	AC'	TTT'	rgg	AAT'	TCC/	AGA	AGAG	CTT:	ГGАC	CTAC	CAT	AGA	CTAA	\Aat	att	cca	atg	jtg	gtga	aagg
721	ato	gta	caa	gct	tgt	gaat	ato	gtaa	aatt	tta	aaa	cta	ttat	cta	aact	aaq	gtgt	act	gaa	attg
781	tc	gtt	ge	ctg	taad	ctgt	gti	tat	cat	ttt	ati	aat	tgtt	aaa	ataa	agt	gta	aaa	atgo	caaa
841	aaa	aaa	aaa	aaa.	aaaa	aaaa	aaa	aaa	aaaa	a										

Figure 2B. The cDNA (SEQ ID. NO:4) and amino acid sequence (SEQ ID. NO:5) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

		1	cc	222	ato	222	cac	atc	caa	300	tat.		~~~	act.	at o	200		~~~	~~~	cccggccagc	
1		-	-	uuu	400	uuu	cgc										-	-			
								М	S				G		S	A	Е	E	K	R	
61	gg	aag		ctg		_	-		_	AAA	GAA	AAA	AGG	ACT	GAG:	rgc/	\GA/	AGA	AAA	GAGA	
14	Т	R	M	М	Ε	Ι	F	S	Ε	T	K	D	V	F	Q	L	K	D	L	E	
121	AC	TCG	CAT	GAT	GGA	AAT	ATT	TTC	rga.	AAC	AAA	AGA!	FGTA	ATT!	rca <i>i</i>	ATTA	AAA	AGA	CTT	GGAG	
34	K	I	Α	P	K	Ε	K	G	1	Т	Α	М	s	V	K	E	V	L	Q	s	
181	ΑA	GAT	TGC	TCC	CAA	AGA	GAA	AGG	CAT'	rac:	rgc'	PAT	STC	AGT	AAA	AGA/	AGTO	CCT	rca.	AAGC	
54	L	v	D	D	G	М	v	D	С	E	R	1	G	т	s	N	Y	Y	W	A	
241	тт	AGT	TGA	TGA	TGG	TAT	GGT	TGA	CTG	rgad	SAG	SAT	CGGZ	AAC'	TTC:	raan	TA:	rta:	rtg	GGCT	
74	F	P	s	K	Α	L	Н	Α	R	K	Н	K	L	Е	v	L	E	s	Q	D	
301	TT	TCC.	AAG	TAA	AGC	тст	TCA'	rgc	AAG	SAA	ACA:	raac	STT	GGA	GTT	гсто	GA.	ATC:	CAC	GGAC	
94	P	G	С	С	F	Н	Е	I	I	K	v	S	Y	Y	R	K	F	W	L	G	
361	СС	TGG	CTG	CTG	СТТ	CCA	TGA	AAT	AAT'	raa <i>i</i>	AGT	CTC	CTAT	гтаз	rag?	\AA/	ATTO	CTG	CTC	GGC	
114	Α	v	Α	Н	Α	С	N	Р	s	Т	L	G	G	*							
421	GC.	AGT	GGC'	TCA	CGC	CTG	TAA	rcc	CAG	CAC	гтт	GGG/	AGGO	CTGA	Aggo	ggg	gcag	gato	caco	gagg	
481	tg	act	ttc	ccc	cac	ccc	cac	atg.	aagt	gca	aga	atg	gagt	tgt	cto	gago	ggaa	agto	caaa	aagc	
541	at	gca	agc	cta	cag	aaa.	agc.	att	gaga	aaa	geta	aaaa	atto	ggc	gat	gto	jaaa	acg	gaag	gage	
601	ga	acc	agg	cta	gca	aaa	gag	ctt	ctt	cad	ette	cgaç	gaco	caaa	agg	gaac	cago	ctaa	aag	gcag	
661	aa	gta	gaa	aaa	tac	aaa	gac	gto	gato	ccg	caaq	gttç	gtg	gaaq	gaaa	atac	gco	caaq	gcaa	aata	
721	aa	gta	gcc	aaa	gaa	gct	gct.	aac	agat	gga	acto	gata	aca	atat	tc	gcaa	taa	aaat	ctt	ggg	
781	CC	aaa	aga.	aaa	ttt	ggg	ttt	gaa	gaaa	aata	aaa	atto	gata	agaa	ctt	ttç	ggaa	atto	cca	gaag	
841	ac	ttt	gac	tac	ata	gac	taa	aata	atto	cat	ggt	ggt	gaa	agga	atgt	aca	ago	ette	gtga	aata	
901	tg	taa	att	tta	aac	tat	tat	cta	acta	aagt	gta	acto	jaat	tgt	cgt	ttç	jcct	gta	act	gtg	
961	tt	tat	cat	ttt.	att.	aat	gtt	aaat	aaa	gto	gtaa	aaat	gca	aaaa	aaaa	aaaa	aaa	aaaa	aaaa	aaaa	
1021	aa	aaa.	aaa																		

App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al. Title: NUCLEIC ACID AND CORRESPONDING PROTEIN

ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
REPLACEMENT SHEET
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Figure 2C. The cDNA (SEQ ID. NO:6) and amino acid sequence (SEQ ID.NO:7) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

1	ccaa	aat	caa	acç	cgt	ccc	ggc	ctg	tcc	cgc	ccc	tct	ccc	caa	gcg	cgg	gcc	cgg	cca	gc
61	ggaa	gcc	cct	geg	ccc	gcg	cca	tgt	caa	aga	aaa	aag	gac	tga	gtg	cag	aag	aaa	aga	ga
121	acto	gca	tga	tgg	aaa	tat	ttt	ctg	aaa	caa	aag	atg	tat	ttc	aat	taa	aag	act	tgg	ag
181	aaga	ttç	ctc	cca	aag	aga	aag	gca	tta	ctg	cta	tgt	cag	taa	aag	aag	tcc	ttc	aaa	gc
241	ttag	ttç	atg	atg	gta	tgg	ttg	act	gtg	aga	gga	tcg	gaa	ctt	cta	att	att	att	ggg	ct
301	tttc	caa	gta	aag	ctc	ttc	atg	caa	gga	aac	ata	agt	tgg	agg	ttc	tgg	aat	ctc	agg	ac
361	cctg	gct	gct	gct	tcc	atg	aaa	taa	tta	aag	tct	cct	att	ata	gaa	aat	tct	ggc	tgg	gc
421	gcag	tgg	ctc	acg	cct	gta	atc	сса	gca	ctt	tgg	gag	gct	gag	gcg	ggc	aga	tca	cga	gg
1							М	K	С	K	М	Е	L	S	E	G	s	Q	K	Н
481	tgac	ttt	ccc	сса	ccc	сса	cAT	<u>G</u> AA	GTG	CAA	GAT	GGA	GTT	GTC	TGA	GGG	AAG	TCA	AAA	GC
15	A	s	L	Q	K	S	I	E	K	Α	K	Ι	G	R	С	E	Т	E	Ε	R
541	ATGC	AAG	CCT	ACA	GAA	AAG	CAT	TGA	GAA	AGC	TAA	AAT	TGG	CCG	ATG	TGA	AAC	GGA	AGA	.GC
35	T	R	L	Α	K	E	L	S	S	L	R	D	Q	R	E	Q	L	K	Α	E
601	GAAC	CAG	GCT	AGC	AAA	AGA	GCT	TTC	TTC	ACT	TCG	AGA	CCA	AAG	GGA	ACA	GCT	AAA	GGC	AG
55	V	E	K	Y	K	D	С	D	P	Q	٧	V	E	E	1	R	Q	Α	N	K
661	AAGT	AGA	AAA	ATA	CAA	AGA	CTG	TGA	TCC	GCA	AGT	TGT	GGA	AGA	AAT	ACG	CCA	AGC	AAA	TA
75	V	A	K	Ε	Α	Α	N	R	W	Т	D	N	Ι	F	Α	I	K	s	W	A
721	AAGT	AGC	CAA	AGA	AGC	TGC	TAA	CAG	ATG	GAC	TGA	TAA	CAT	ATT	CGC	AAT	AAA	ATC	TTG	GG
95	K	R	K	F	G	F	E	E	N	K	I	D	R	T	F	G	I	P	E	D
781	CCAA	AAG	AAA	ATT	TGG	GTT	TGA	AGA	AAA	TAA.	AAT	rga	TAG	AAC	TTT	TGG.	AAT	TCC	AGA	AG
115	F	D	Y	I	D	*														
841	ACTT	TGA	CTA	CAT	AGA	CTA	Aaa	tat	tcc	atg	gtg	gtg	aag	gat	gta	caa	gct	tgt	gaa	ta
901	tgta	aat	ttt	aaa	cta	tta	tct	aac	taa	gtg	tac	tga.	att	gtc	gtt	tgc	ctg	taa	ctg	tg
961	ttta	tca	ttt	tat	taa	tgt	taa	ata	aag	tgt	aaa	atg	caa	aaa	aaa	aaa	aaa	aaa	aaa	aa

1021 aaaaaaaa

Figure 2D. The cDNA (SEQ ID. NO:8) and amino acid sequence (SEQ ID. NO:9) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

1	cc	aaa	atc	aaa	cgc	gtc	cgg	gcc	tgt	ccc	gcc	cct	ctc	ccc	aag	cgc	ggg	ccc	ggc	cage
1								М	s	K	K	K	G	L	s	А	Ε	E	K	R
61	gg	aag	ccc	ctg	cgc	ccg	cgc	c <u>AT</u>	GTC	AAA	GAA	AAA	AGG	ACT	GAG	TGC	AGA	AGA	AAA	GAGA
14	T	R	М	М	Ε	Ι	F	s	E	T	K	D	V	F	Q	L	K	D	L	E
121	AC	TCG	CAT	GAT	'GGA	AAT	ATT	TTC	TGA	AAC	AAA	AGA	TGT	ATT	TCA	ATT	AAA	AGA	CTT	GGAG
34	K	Ι	А	P	K	Ε	K	G	I	Т	А	М	s	V	K	E	v	L	Q	s
181	AA	GAT	TGC	TCC	CAA	AGA	GAA	AGG	CAT	TAC	TGC	TAT	GTC	AGT	AAA	AGA	AGT	CCT	TCA	AAGC
54	L	V	D	D	G	М	V	D	С	E	R	Ι	G	T	S	N	Y	Y	W	A
241	TT.	AGT	TGA	TGA	TGG	TAT	GGT	TGA	CTG	TGA	GAG	GAT	CGG	AAC	TTC	TAA	TTA	TTA	TTG	GGCT
74	F	P	s	K	Α	L	Н	А	R	K	Н	K	L	E	V	L	Ε	s	Q	L
301	TT	TCC	AAG	TAA	AGC	TCT	TCA	TGC	AAG	GAA	ACA	TAA	GTT	GGA	GGT	TCT	GGA	ATC	TCA	GTTG
94	s	Е	G	S	Q	K	Н	А	S	L	Q	K	s	1	E	K	A	K	I	G
361	TC	TGA	GGG	AAG	TCA	AAA	.GCA	TGC	AAG	CCT	ACA	GAA	AAG	CAT	TGA	GAA	AGC	TAA	AAT	TGGC
114	R	С	Ε	T	Α	K	Q	I	K	*										
421	CG.	ATG	TGA	AAC	GGC	CAA	GCA.	AAT	AAA	GTA	GCC	aaa	gaa	gct	gct	aac	aga	tgg	act	gata
481	ac.	ata	ttc	gca	ata	aaa	tct	tgg	gcc	aaa	aga	aaa	ttt	ggg	ttt	gaa	gaa	aat	aaa	attg
541	at.	aga	act	ttt	gga	att	cca	gaa	gac	ttt	gac	tac	ata	gac	taa	aat	att	сса	tgg	tggt
601	ga	agg	atg	tac	aag	ctt	gtg	aat	atg	taa	att	tta	aac	tat	tat	cta	act	aag	tgt	actg
661	aa	ttg	tcg	ttt	gcc	tgt	aac	tgt	gtt	tat	cat	ttt	att	aat	gtt	aaa	taa	agt	gta	aaat
721	gc	aaa	aaa	aaa	aaa	aaa	aaa	aaa	aaa	aaa	aaa									

App No.: 10/087,190
Inventor: Pia M. CHALLITA-EID et al.
Title: NUCLEIC ACID AND CORRESPONDING PROTEIN
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Figure 2E. The cDNA (SEQ ID. NO:10) and amino acid sequence (SEQ ID. NO:11) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

1 ccaaaatcaaacgcgtccgggcctgtcccgcccctctccccaagcgcgggcccggccagc 1 M S K K K G L S A E E K R 61 ggaagecetgegeeggecATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA 14 T R M M E I F S E T K D V F Q L K D L E 121 ACTCGCATGATGGAAATATTTTCTGAAACAAAGATGTATTTCAATTAAAAGACTTGGAG 34 K I A P K E K G I T A M S V K E V T. O S 181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC 54 L V D D G M V D C E R I G T S N Y Y W A 241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT 74 F P S K A L H A R K H K L E V L E S 301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG 94 S E G S O K H A S L O K S I E K A K T 361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC ETEERTRLAKELSSLR 421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA EOLKAEVEKYKDCDPOVV 481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA HNIFAIKSWAKRKFGF 541 GAAATACATAACATATTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAA 174 N K I D R T F G I P E D F D Y I D 601 AATAAAATTGATAGAACTTTTGGAATTCCAGAAGACTTTGACTACATAGACTAAaatatt 661 ccatggtggtgaaggatgtacaagcttgtgaatatgtaaattttaaactattatctaact 721 aagtgtactgaattgtcgtttgcctgtaactgtgtttatcattttattaatgttaaataa

Figure 2F. The cDNA (SEQ ID. NO:12) and amino acid sequence (SEQ ID. NO:13) of 121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

1 gttttctgtattgtaatatgtagagcacattccagaactgctcagtttcgagttacctaa 61 tqqatcttcactqtgtgccaattagtcgatttctqtqaaaacqccccqqtttctqccaaa 121 gggcaggagtcgctgctcttgtgccgggtqctqctqqttqtqtaqqqcqctqttqcttt 181 ttaaggacgctctgcactgaattaggcttcctcgtqqqtcatqatcagttaaqtcctqtc 1 MMEIFSE 241 aaagaaaaaaggactgagtgcagaagaaaagagaactcgcATGATGGAAATATTTTCTGA TKDVFQLKDLEKIAPKEKGI 301 AACAAAAGATGTATTTCAATTAAAAGACTTGGAGAAGATTGCTCCCAAAGAGAAAGGCAT TAMSVKEVLOSTVDDGMVDC 361 TACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGCTTAGTTGATGATGGTATGGTTGACTG E R I G T S N Y Y W A F P S K A T. H A R 421 TGAGAGGATCGGAACTTCTAATTATTATTGGGCTTTTCCAAGTAAGCTCTTCATGCAAG K H K L E V L E S O L S E G S O K H A S 481 GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAGTCAAAAGCATGCAAG LOKSIEKAKIGRCETEERTR 541 CCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGCGAACCAG LAKELSSLRDOREOLKAEVE 601 GCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAGAAGTAGA K Y K D C D P O V V E E I R O A N K V A 661 AAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAATACGCCAAGCAAATAAAGTAGC K E A A N R W T D N I F A I K S W A K 721 CAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGGCCAAAAG FGFEENKIDRTFGI 781 AAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGAATTCCAGAAGACTTTGA Y I D * 841 CTACATAGACTAAaatattccatggtggtgaaggatgtacaagcttgtgaatatgtaaat 901 tttaaactattatctaactaagtgtactgaattgtcgtttgcctgtaactgtgtttatca 961 ttttattaatgttaaataaagtgtaaaatgcagatgttcttcaccccttttggtagaaca 1021 aaagcaggatgataaccatatccccccagtgctcatcaaagtaggacactaaaaatccat 1081 ccatctcagtcaaagtcgagcggccgcgaatttagtagtagtagcggccgctctagagga 1141 tccaagcttacgtacgcgtgcatgcgacgtcatagctcttctatagtgtcacctaaattc 1201 aagtt

Figure 3:

Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO:14). The 121P1F1 protein has 205 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LOSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSOKH ASLOKSIEKA KIGRCETEER
- 121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIRQANK VAKEAANRWT DNIFAIKSWA
- 181 KRKFGFEENK IDRTFGIPED FDYID

Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO:15). The 121P1F1 splice variant 1A protein has 126 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYYRKF WLGAVAHACN
- 121 PSTLGG

Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO:16). The 121P1F1 splice variant 1B protein has 119 amino acids.

- 1 MKCKMELSEG SOKHASLOKS IEKAKIGRCE TEERTRLAKE LSSLRDOREO LKAEVEKYKD
- 61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKRKFGF EENKIDRTFG IPEDFDYID

Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO:17). The 121P1F1 splice variant 2 protein has 122 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LOSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKQ
- 121 IK

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO:18). The 121P1F1 splice variant 3 protein has 190 amino acids.

- 1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
- 61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
- 121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIHNIFA IKSWAKRKFG FEENKIDRTF
- 181 GIPEDFDYID

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO:19). The 121P1F1 splice variant 4 protein has 190 amino acids.

- 1 MMEIFSETKD VFQLKDLEKI APKEKGITAM SVKEVLQSLV DDGMVDCERI GTSNYYWAFP
- 61 SKALHARKHK LEVLESQLSE GSQKHASLQK SIEKAKIGRC ETEERTRLAK ELSSLRDORE
- 121 QLKAEVEKYK DCDPQVVEEI RQANKVAKEA ANRWTDNIFA IKSWAKRKFG FEENKIDRTF
- 181 GIPEDFDYID

App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al. Title: NUCLEIC ACID AND CORRESPONDING PROTEIN

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Figure 4A

Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

1 15 16

A) CLUSTAL W alignment of 121P1F1 and variants 1-3. (SEO ID NOS: 3, 5, 7, 9 and 11)

121P1F01 sv1A sv1B sv-2 sv-3	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKE
121P1F01 sv1A sv1B sv-2 sv-3	VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-HASLQKS-I VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQDP-GCCF-HEIIKVSYY QLKAEVEK-YKDCDPQVVEEIRQANKVAKEARRWTDNIFAIKSWAKRKFGFEENKID VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-HASLQKS-I VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-HASLQKS-I
121PTF01 sv1A sv1B sv-2 sv-3	EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAAN RKFWLGAVAHACNPSTLGG
121P1F01 sv1A sv1B sv-2 sv-3	RWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDFDYID

Figure 4B

B) Clustal alignment of 121P1F1 and variants 1A and 4 (SEQ ID NOS 3, 13 and 5)

30 31

- 1	121P1F01	MSKKKGLSAEEKRTR	MMEIFSETKDVFQLK	DLEKIAPKEKGITAM	SVKEVLQSLVDDGMV	DCERIGTSNYYWAFP	SKALHARKHKLEVLE
	sv-4		MMEIFSETKDVFQLK				
3	sv-IA	MSKKKGLSAEEKRTR	MMEIFSETKDVFQLK	DLEKIAPKEKGITAM	SVKEVLQSLVDDGMV	DCERIGTSNYYWAFP	SKALHARKHKLEVLE
		91 105	106 120	I21 I35	136 I50	ISI I65	166 180
1	121P1F01	SQLSEGSQKHASLQK	SIEKAKIGRCETEER	TRLAKELSSLRDQRE	QLKAEVEKYKDCDPO	VVEEIROANKVAKEA	ANRWIDNIFAIKSWA
- 2	sv-4	SQLSEGSQKHASLQK	SIEKAKIGRCETEER	TRLAKELSSLRDORE	QLKAEVEKYKDCDPO	VVEEIROANKVAKEA	ANRWIDNIFAIKSWA
1	sv-lA	SQDPGCCFHEIIKVS	YYRKFWLG		AVAHACNPS	TLGG	
		181 195	196 210	211			
1	121P1F01	KRKFGFEENKIDRTF	GIPEDFDYID 205				
- 2	sv-4	KRKEGFEENKIDRTE	GIPEDFDYID 190				
-							

App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al. Title: NUCLEIC ACID AND CORRESPONDING PROTEIN

ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc.
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Figure 4C

C) Alignment of 121P1F1 and variant 1 (SEQ ID NO:20) with human GAJ (SEQ ID NO:21) Identities = 205/205 (100%), Positives = 205/205 (100%)

- 121P1: 1 MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
 MSKKKGLSAEEKRTRMMEIFSETKDVFOLKDLEKIAPKEKGITAMSVKEVLOSLVDDGMV
- Sbjct: 1 MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
- 121P1: 61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
- DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER
- Sbjct: 61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
- 121P1: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
- TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA Sbjct: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
- 121P1: 181 KRKFGFEENKIDRTFGIPEDFDYID 205
 - KRKFGFEENKIDRTFGIPEDFDYID
- Sbjct: 181 KRKFGFEENKIDRTFGIPEDFDYID 205

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Figure 4D

D) Alignment of 121P1F1 and variant 1 (SEQ ID NO:22) with closest mouse homolog, a hypothetical 24.2 KDa protein. (SEQ ID NO:23) Identities = 183/205 (89%), Positives = 193/205 (93%)

121P1:	1	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV	60
Sbjct:	1	MSKK+GLS EEKRTRMMEIF ETKDVFQLKDLEK+APKEKGITAMSVKEVLQSLVDDGMV MSKKRGLSGEEKRTRMMEIFFETKDVFQLKDLEKLAPKEKGITAMSVKEVLQSLVDDGMV	60
121P1:	61	${\tt DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER}$	120
Sbjct:	61	DCERIGTSNYYWAFPSKALHARK KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER DCERIGTSNYYWAFPSKALHARKRKLEALNSQLSEGSQKHADLQKSIEKARVGRQETEER	120
121P1:	121	TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA	180
		LAKEL S RDQR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANRWTDNIFAIKSWA AMLAKELFSFRDQRQQLKAEVEKYRECDPQVVEEIREANKVAKEAANRWTDNIFAIKSWA	

121P1: 181 KRKFGFEENKIDRTFGIPEDFDYID 205 KRKFGFEE+KID+ FGIPEDFDYID

Sbjct: 181 KRKFGFEESKIDKNFGIPEDFDYID 205

Figure 4E

```
E) Alignment of 121P1F1 and variant 1 (SEO ID NO:24)
  with>gi|1175412|sp|009739|YA53 SCHPO HYPOTHETICAL 24.2 KD
  PROTEIN C13A11.03 IN CHROMOSOME I (SEO ID NO:25)
   gi|7490680|pir||T37610 hypothetical coiled-coil protein -
   fission veast
   (Schizosaccharomyces pombe)
    qi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil
   protein [Schizosaccharomyces pombe]
          Length = 210
 Score = 121 bits (305), Expect = 5e-27
 Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps =
6/202 (2%)
Query: 5
KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLOSLVDDGMVDCER 64
           KGLS EKR R+ IF ++KD FOLK++EK+ K K I
+VK+VLOSLVDD +V
                 E+
Sbict: 4
           KGLSLAEKRRRLEAIFHDSKDFFOLKEVEKLGSK-
KOIVLOTVKDVLOSLVDDNIVKTEK 62
Query: 65 IGTSNYYWAFPSKALHARKHKLEVLESOLSEGSOKHASLOKSIEKAKIGR--
--CETEER 120
           IGTSNYYW+FPS A +R+ L L++QL + QK +L ++I
                                                         K R
Sbict: 63
IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN
122
Query: 121
TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIROANKVAKEAANRWTDNIFAIKSWA
180
               + L + + + LK ++
                                   C+P+ E + K
                                                      EAAN WTD
I + ++
Sbict: 123
QYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC
182
Ouerv: 181 KRKFGFEENKIDRTFGIPEDFD 202
            R G + N+I
                           TPED D
Sbict: 183 -RDMGADTNOIREYCSIPEDLD 203
```

Figure 5A 121P1F1 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

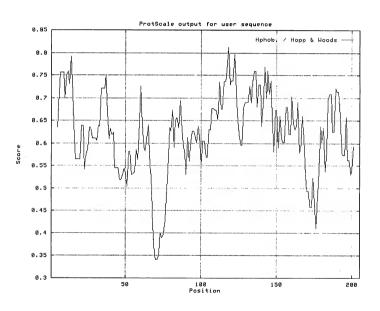


Figure 5B 121P1F1 variant 1a Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

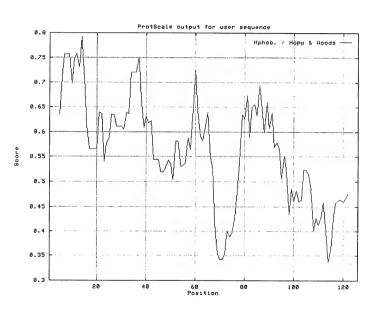


Figure 6A 121P1F1 Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

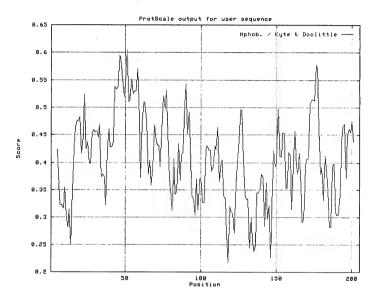


Figure 6B 121P1F1 variant 1a Hydropathicity Profile (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

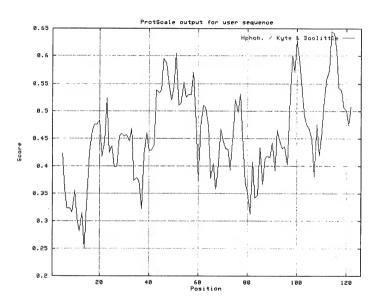


Figure 7A 121P1F1 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

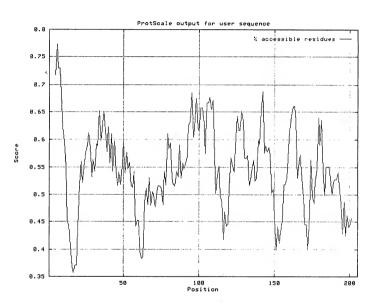


Figure 7B 121P1F1 variant 1a % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

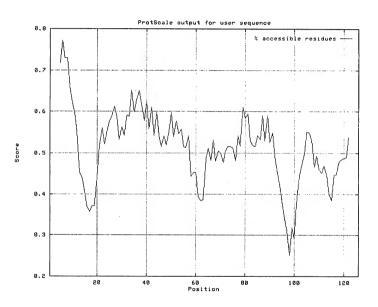


Figure 8A 121P1F1 Average Flexibility Profile (Rhaskaran B. Pannusurum B.K. 1088)

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

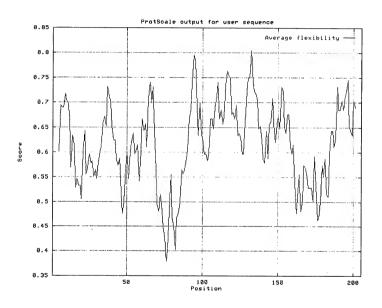


Figure 8B 121P1F1 variant 1a Average Flexibility Profile (Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

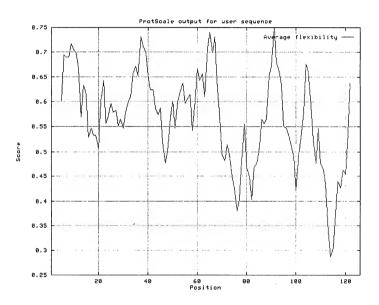


Figure 9A 121P1F1 Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

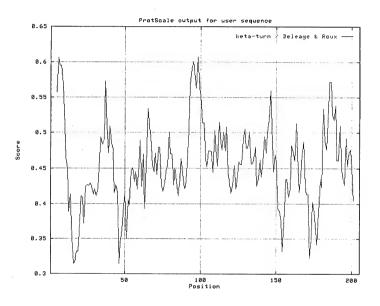
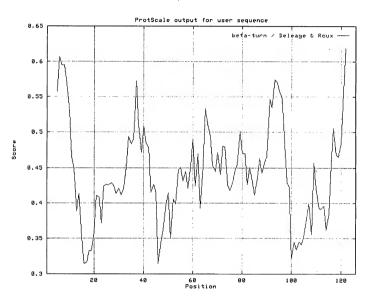
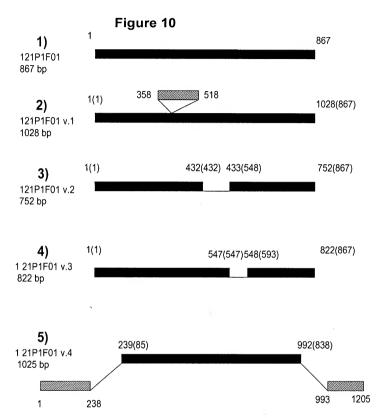


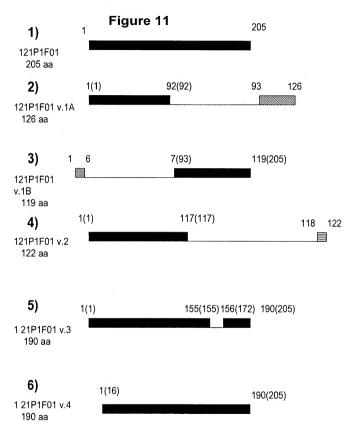
Figure 9B 121P1F1 variant 1a Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



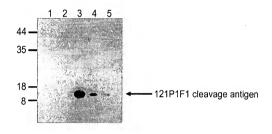


Note: Numbers in "()" correspond to those of the original sequence. Black box shows the same sequence as the original one. SNPs are indicated above the box,

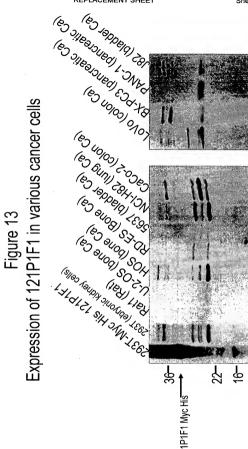


Note: Numbers in "()" correspond to those of the original sequence. Black box shows the same sequence as the original one. Single amino acid variations are indicated above the box.

Figure 12
Specific recognition of 121P1F1 antigen by anti-121P1F1 pAb



1. Pre-immune	1:100
2. Pre-immune	1:1,600
3. Anti-121P1F1 serum	1:100
4. Anti-121P1F1 serum	1:400
5. Anti-121P1F1 serum	1:1,600



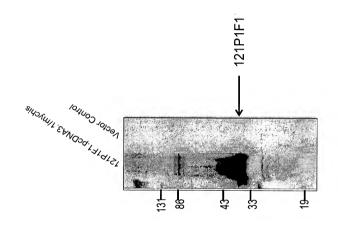
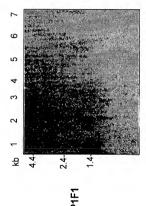


Figure 15 121P1F1 Androgen Regulation In Vivo

App No.: 10/087,190 Docket No.: 511582003420 Inventor: Pia M. CHALLITA-EID et al. Title: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 121P1F1 USEFUL IN TREATMENT AND, etc. REPLACEMENT SHEET Sheet 28 of 36

1. LAPC-9AD Day 0
2. LAPC-9AD Day 0
3. LAPC-9AD Day 7
4. LAPC-9AD Day 7
5. LAPC-9AD Day 15
6. LAPC-9AD Day 15
7. LAPC-9AD Day 15







TMPRSS2

Figure 16A

Secondary structure prediction of 121P1F1

	10	20	30	40	50	09	7.0
	_		_		_		_
MSKKKGL	SAEEKRTRMME	EIFSETKDVFÇ	QLKDLEKIAP!	KEKGITAMSVJ	KEVLQSLVDD	MSKKKGLSAEEKRIRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNY	Ϋ́
0000000	сһһһһһһһһһ	հերհերուհերհե	ոհհհհհհհե	сссрррррр	հերհերհերե	сссссссирининининининининининининининисссссинининининининининини	Ö
YWAFPSK	ALHARKHKLEN	VLESQLSEGS(DKHASLQKSII	EKAKIGRCETI	EERTRLAKEL	YWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREQLKAE	Æ
eeeccchl	һһһһһһһссеһ	hhhhcccccc	լկկկկկկկկկրի 	ռիհիշշշշի	հերհերհերե	ееесссийнининссенининссссссинининининининининини	Ч
VEKYKDCI	VEKYKDCDPQVVEEIRQANKVAKEAANRWTDNI FAIKSWAKRKFGFEENKIDRTFGIPEDFDYID	ANKVAKEAANI	RWTDNIFAIK	SWAKRKFGFEI	ENKIDRTFGI	PEDFDYID	
hhhhccc	ининссссснинининининининининининининини	դրրրիրիրիրի 1	իրերերերե	ոհհհհհե	heceeeeee	2222222	

Alpha helix (h): 61.95% Extended strand (e): 1.95% Random coil (c): 36.10%

Figure 16B

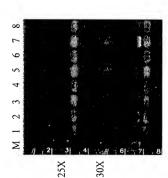
Secondary structure prediction of variant 1a

10	20	30	40	20	09	70
	and a	_	_	_	_	_
RTF	MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNY	VFQLKDLEK]	IAPKEKGITAN	MSVKEVLQSLA	VDDGMVDCER	IGTSNY
hhk	ссссссьнинининининининининининининининисссссонининини	կրրրերիր	occccchhh!	ղորհիհիհիհի	hccccchhc	000000
KHk	YWAFPSKALHARKHKLEVLESQDPGCCFHEIIKVSYYRKFWLGAVAHACNPSTLGG	CCFHEIIKVS	SYYRKFWLGAN	VAHACNPSTLO	36	
SS	ееесссирнинисссееееесссссирнинининининисеессссссс	сһһһһһһһ	hhhhhhhcce	Secccccccc	ပ္ပ	

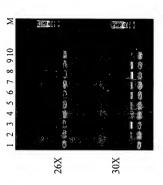
Alpha helix (h): 50.79% Extended strand (e): 7.94% Random coil (c): 41.27%

Figure 17 Expression of 121P1F1 by RT-PCR

A. Human normal tissues



B. Patient tumor specimens



6) Bladder cancer pool 7) Kidney cancer pool 8) Colon cancer pool 2) VP2 1) VP1 3) XP

5) Small Int.

1) Colon 2) Ovary 3) Leuk. 4) Prost.

6) Spleen 7) Testis

- 9) Lung tumor 4) Normal prostate
- 5) Prostate cancer pool 10) H2O

8) Thymus

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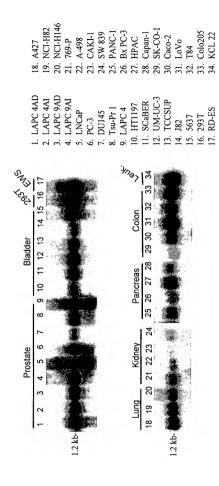
REPLACEMENT SHEET

Figure 18 Expression of 121P1F1 in normal human tissues ω ဖ 2 က ž, 2 7.5 4.4 2.4-4 Ω ∞ 9 2 4 1. Heart က 2 5 9.5 2.4 4.4 4

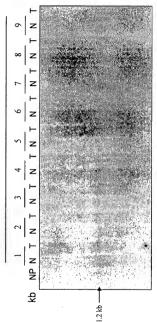
4



Figure 19 Expression of 121P1F1 in Multiple Cancer Cell lines



Patient sample numbers



NP = Normal Prostate = Normal= Tumor ≥ ⊦

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App No.: 10/087,190 Docket No.: 51158200
Inventor: Pia M. CHALLITA-EID et al.
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Figure 21 Expression of 121P1F1 in Kidney, Breast, Cervical and Stomach Patients Samples as well as Cancer Cell lines



breast

stomach

cervix



N = normal adjacent tissue RNA T = tumor RNA

Cancer cell lines are:

Daudi (Burkitt's lymphoma) HeLa (cervical carcinoma) HL-60 (PML) K562 (CML)

SW480 (colorectal carcinoma) MOLT-4 (lymphoblastic leuk.) Raji (Burkitt's lymphoma) A549 (lung carcinoma) G361 (melanoma)



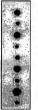


Figure 22 Androgen Regulation of 121P1F1

5

